

Sequence Listing

<110> Baker, Kevin
 Botstein, David
 Eaton, Dan
 Ferrara, Napoleone
 Filvaroff, Ellen
 Gerritsen, Mary
 Goddard, Audrey
 Godowski, Paul
 Grimaldi, Christopher
 Gurney, Austin
 Hillan, Kenneth
 Kljavin, Ivar
 Napier, Mary
 Roy, Margaret
 Tumas, Daniel
 Wood, William

<120> SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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FOUO ECH-60

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<151> March 2, 2000

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 35 40 45
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 50 55 60
 Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
 65 70 75
 Phe Gly Cys Gln Cys Tyr Ser Arg Val Val His Cys Ser Asp Leu
 80 85 90
 Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met
 95 100 105
 Leu Asp Leu Gln Asn Asn Lys Ile Lys Glu Ile Lys Glu Asn Asp
 110 115 120
 Phe Lys Gly Leu Thr Ser Leu Tyr Gly Leu Ile Leu Asn Asn Asn
 125 130 135
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 140 145 150
 Leu Arg Arg Leu Tyr Leu Ser His Asn Gln Leu Ser Glu Ile Pro
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 170 175 180
 Lys Val Lys Lys Ile Gln Lys Asp Thr Phe Lys Gly Met Asn Ala
 185 190 195
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Glu	Leu	Glu	Asp	Phe	Lys	Arg	Tyr	Lys	Glu	Leu	Gln	Arg	Leu	Gly
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Ala Val Gly Ile Cys Pro Gly Leu Gly	Ala Arg Gly Ala His Met	
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Ala Leu Val Leu Pro Pro Val Lys Ser	Gln Ala Ala Gly His Ala	
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650	655	660

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Cys	Ala	Val	Cys	Thr 815	Cys	Lys	Gly	Gly	Thr 820	Gly	Glu	Val	His	Cys 825
Glu	Lys	Val	Gln	Cys 830	Pro	Arg	Leu	Ala	Cys 835	Ala	Gln	Pro	Val	Arg 840
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Ala	His	Pro	Gln	Leu 860	Gly	Asp	Pro	Met	Gln 865	Ala	Asp	Gly	Pro	Arg 870
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His	Pro	Ser	Val	Pro 890	Pro	Phe	Gly	Glu	Met 895	Ser	Cys	Ile	Thr	Cys 900
Arg	Cys	Gly	Ala	Gly 905	Val	Pro	His	Cys	Glu 910	Arg	Asp	Asp	Cys	Ser 915
Leu	Pro	Leu	Ser	Cys 920	Gly	Ser	Gly	Lys	Glu 925	Ser	Arg	Cys	Cys	Ser 930
Arg	Cys	Thr	Ala	His 935	Arg	Arg	Pro	Pro	Glu 940	Thr	Arg	Thr	Asp	Pro 945
Glu	Leu	Glu	Lys	Glu	Ala	Glu	Gly	Ser						

<210> 8
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide probe

 <400> 8
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 <210> 9
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 9
 cggacgcgtg gggcctgcmc acccagct 28

 <210> 10
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 10
 gccgctcccc gaacgggcag cggctccttc tcagaa 36

 <210> 11
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 11
 ggcgcacagc acgcagcgca tcaccccgaa tggctc 36

 <210> 12
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 12
 gtgctgccca tccgttctga gaagga 26

 <210> 13

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tgaagaatac	gatgcttgcc	agaggaaacc	ttgccaaaac	aacgcgagct	1200
gtattgatgc	aaatgaaaag	caagatggga	gcaatttcac	ctgtgtttgc	1250
cttcctgggt	atactggaga	gctttgccag	tccaagattg	attactgcat	1300
cctagaccca	tgcagaaatg	gagcaacatg	cattttccagt	ctcagtggat	1350
tcacctgcca	gtgtccagaa	ggatacttcg	gatctgcttg	tgaagaaaag	1400
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ccatggcctc	tactgtgagg	aggaatataa	tgagtgcctc	tccgtccat	1650
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ctcaccaaca	tgccacggca	ctccctctac	atcatcattg	gagccctctg	2050
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gatgagatac	tacactcatt	taaatatttt	taagaaaata	aaaagcttaa	2400
gaaatttaaa	atgctagctg	ctcaagagtt	ttcagtagaa	tatttaagaa	2450
ctaattttct	gcagcttttta	gtttggaaaa	aatattttta	aaacaaaatt	2500

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Cys	Ile	Cys	Asn	Glu 125	Gly	Tyr	Glu	Gly	Pro 130	Asn	Cys	Glu	Gln	Ala 135
Leu	Pro	Ser	Leu	Pro 140	Ala	Thr	Gly	Trp	Thr 145	Glu	Ser	Met	Ala	Pro 150
Arg	Gln	Leu	Gln	Pro 155	Val	Pro	Ala	Thr	Gln 160	Glu	Pro	Asp	Lys	Ile 165
Leu	Pro	Arg	Ser	Gln 170	Ala	Thr	Val	Thr	Leu 175	Pro	Thr	Trp	Gln	Pro 180
Lys	Thr	Gly	Gln	Lys 185	Val	Val	Glu	Met	Lys 190	Trp	Asp	Gln	Val	Glu 195
Val	Ile	Pro	Asp	Ile 200	Ala	Cys	Gly	Asn	Ala 205	Ser	Ser	Asn	Ser	Ser 210
Ala	Gly	Gly	Arg	Leu 215	Val	Ser	Phe	Glu	Val 220	Pro	Gln	Asn	Thr	Ser 225
Val	Lys	Ile	Arg	Gln 230	Asp	Ala	Thr	Ala	Ser 235	Leu	Ile	Leu	Leu	Trp 240
Lys	Val	Thr	Ala	Thr 245	Gly	Phe	Gln	Gln	Cys 250	Ser	Leu	Ile	Asp	Gly 255
Arg	Ser	Val	Thr	Pro 260	Leu	Gln	Ala	Ser	Gly 265	Gly	Leu	Val	Leu	Leu 270
Glu	Glu	Met	Leu	Ala 275	Leu	Gly	Asn	Asn	His 280	Phe	Ile	Gly	Phe	Val 285
Asn	Asp	Ser	Val	Thr 290	Lys	Ser	Ile	Val	Ala 295	Leu	Arg	Leu	Thr	Leu 300
Val	Val	Lys	Val	Ser 305	Thr	Cys	Val	Pro	Gly 310	Glu	Ser	His	Ala	Asn 315
Asp	Leu	Glu	Cys	Ser 320	Gly	Lys	Gly	Lys	Cys 325	Thr	Thr	Lys	Pro	Ser 330
Glu	Ala	Thr	Phe	Ser 335	Cys	Thr	Cys	Glu	Glu 340	Gln	Tyr	Val	Gly	Thr 345
Phe	Cys	Glu	Glu	Tyr 350	Asp	Ala	Cys	Gln	Arg 355	Lys	Pro	Cys	Gln	Asn 360
Asn	Ala	Ser	Cys	Ile 365	Asp	Ala	Asn	Glu	Lys 370	Gln	Asp	Gly	Ser	Asn 375
Phe	Thr	Cys	Val	Cys 380	Leu	Pro	Gly	Tyr	Thr 385	Gly	Glu	Leu	Cys	Gln 390
Ser	Lys	Ile	Asp	Tyr 395	Cys	Ile	Leu	Asp	Pro 400	Cys	Arg	Asn	Gly	Ala 405

Thr Cys Ile Ser	Ser Leu Ser Gly Phe	Thr Cys Gln Cys Pro Glu	410	415	420
Gly Tyr Phe Gly	Ser Ala Cys Glu Glu	Lys Val Asp Pro Cys Ala	425	430	435
Ser Ser Pro Cys	Gln Asn Asn Gly Thr	Cys Tyr Val Asp Gly Val	440	445	450
His Phe Thr Cys	Asn Cys Ser Pro Gly	Phe Thr Gly Pro Thr Cys	455	460	465
Ala Gln Leu Ile	Asp Phe Cys Ala Leu	Ser Pro Cys Ala His Gly	470	475	480
Thr Cys Arg Ser	Val Gly Thr Ser Tyr	Lys Cys Leu Cys Asp Pro	485	490	495
Gly Tyr His Gly	Leu Tyr Cys Glu Glu	Glu Tyr Asn Glu Cys Leu	500	505	510
Ser Ala Pro Cys	Leu Asn Ala Ala Thr	Cys Arg Asp Leu Val Asn	515	520	525
Gly Tyr Glu Cys	Val Cys Leu Ala Glu	Tyr Lys Gly Thr His Cys	530	535	540
Glu Leu Tyr Lys	Asp Pro Cys Ala Asn	Val Ser Cys Leu Asn Gly	545	550	555
Ala Thr Cys Asp	Ser Asp Gly Leu Asn	Gly Thr Cys Ile Cys Ala	560	565	570
Pro Gly Phe Thr	Gly Glu Glu Cys Asp	Ile Asp Ile Asn Glu Cys	575	580	585
Asp Ser Asn Pro	Cys His His Gly Gly	Ser Cys Leu Asp Gln Pro	590	595	600
Asn Gly Tyr Asn	Cys His Cys Pro His	Gly Trp Val Gly Ala Asn	605	610	615
Cys Glu Ile His	Leu Gln Trp Lys Ser	Gly His Met Ala Glu Ser	620	625	630
Leu Thr Asn Met	Pro Arg His Ser Leu	Tyr Ile Ile Ile Gly Ala	635	640	645
Leu Cys Val Ala	Phe Ile Leu Met Leu	Ile Ile Leu Ile Val Gly	650	655	660
Ile Cys Arg Ile	Ser Arg Ile Glu Tyr	Gln Gly Ser Ser Arg Pro	665	670	675
Ala Tyr Glu Glu	Phe Tyr Asn Cys Arg	Ser Ile Asp Ser Glu Phe	680	685	690
Ser Asn Ala Ile	Ala Ser Ile Arg His	Ala Arg Phe Gly Lys Lys			

695	700	705
Ser Arg Pro Ala Met Tyr Asp Val Ser Pro Ile Ala Tyr Glu Asp		
710	715	720
Tyr Ser Pro Asp Asp Lys Pro Leu Val Thr Leu Ile Lys Thr Lys		
725	730	735

Asp Leu

<210> 16
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 16
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 17
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 17
 caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 18
 <211> 508
 <212> DNA
 <213> Homo Sapien

<400> 18
 ctctggaagg tcacggccac aggattccaa cagtgtctcc tcatagatgg 50
 acgaaagtgt gacccccctt tcaggctttc aggggggactg gtcctcctgg 100
 aggagatgct cgccttgagg aataatcact ttattgggtt tgtgaatgat 150
 tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggggaaggt 200
 cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagtgttcag 250
 gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttctgtacc 300
 tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350
 gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400
 aagatgggag caatttcacc tgtgtttgcc ttctgggtta tactggagag 450
 ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500

[illegible]

<400> 19

taggggag 508

<220>

<400> 20

<210> 21

<211> 24

<212> DNA

<220>

<400> 21

<210> 22

<211> 69

<212> DNA

<220>

Variable	Mean	SD	Min	Max
Age	38.5	12.5	25	65
Gender	0.5	0.5	0	1
Marital status	0.7	0.5	0	1
Education	12.5	2.5	9	16
Income	1500	500	500	3000
Health status	0.8	0.4	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.6	0.5	0	1
Depression score	0.4	0.5	0	1
Life satisfaction	0.7	0.5	0	1
Quality of life	0.8	0.4	0	1
Healthcare utilization	0.6	0.5	0	1
Health insurance status	0.9	0.3	0	1
Healthcare access	0.7	0.5	0	1
Healthcare cost	1000	300	500	2000
Healthcare quality	0.8	0.4	0	1
Healthcare satisfaction	0.7	0.5	0	1
Healthcare accessibility	0.6	0.5	0	1
Healthcare affordability	0.5	0.5	0	1
Healthcare effectiveness	0.8	0.4	0	1
Healthcare safety	0.9	0.3	0	1
Healthcare reliability	0.7	0.5	0	1
Healthcare transparency	0.6	0.5	0	1
Healthcare accountability	0.5	0.5	0	1
Healthcare integrity	0.8	0.4	0	1
Healthcare honesty	0.9	0.3	0	1
Healthcare fairness	0.7	0.5	0	1
Healthcare equity	0.6	0.5	0	1
Healthcare justice	0.5	0.5	0	1
Healthcare freedom	0.8	0.4	0	1
Healthcare security	0.9	0.3	0	1
Healthcare privacy	0.7	0.5	0	1
Healthcare confidentiality	0.6	0.5	0	1
Healthcare professionalism	0.8	0.4	0	1
Healthcare competence	0.9	0.3	0	1
Healthcare skillfulness	0.7	0.5	0	1
Healthcare knowledge	0.6	0.5	0	1
Healthcare experience	0.5	0.5	0	1
Healthcare expertise	0.8	0.4	0	1
Healthcare specialization	0.9	0.3	0	1
Healthcare certification	0.7	0.5	0	1
Healthcare accreditation	0.6	0.5	0	1
Healthcare regulation	0.5	0.5	0	1
Healthcare supervision	0.8	0.4	0	1
Healthcare monitoring	0.9	0.3	0	1
Healthcare evaluation	0.7	0.5	0	1
Healthcare assessment	0.6	0.5	0	1
Healthcare review	0.5	0.5	0	1
Healthcare audit	0.8	0.4	0	1
Healthcare inspection	0.9	0.3	0	1
Healthcare investigation	0.7	0.5	0	1
Healthcare inquiry	0.6	0.5	0	1
Healthcare research	0.5	0.5	0	1
Healthcare study	0.8	0.4	0	1
Healthcare analysis	0.9	0.3	0	1
Healthcare examination	0.7	0.5	0	1
Healthcare observation	0.6	0.5	0	1
Healthcare documentation	0.5	0.5	0	1
Healthcare record-keeping	0.8	0.4	0	1
Healthcare data management	0.9	0.3	0	1
Healthcare information systems	0.7	0.5	0	1
Healthcare technology	0.6	0.5	0	1
Healthcare innovation	0.5	0.5	0	1
Healthcare development	0.8	0.4	0	1
Healthcare improvement	0.9	0.3	0	1
Healthcare optimization	0.7	0.5	0	1
Healthcare enhancement	0.6	0.5	0	1
Healthcare advancement	0.5	0.5	0	1
Healthcare progress	0.8	0.4	0	1
Healthcare growth	0.9	0.3	0	1
Healthcare expansion	0.7	0.5	0	1
Healthcare diversification	0.6	0.5	0	1
Healthcare globalization	0.5	0.5	0	1
Healthcare internationalization	0.8	0.4	0	1
Healthcare cross-border	0.9	0.3	0	1
Healthcare transnational	0.7	0.5	0	1
Healthcare multinational	0.6	0.5	0	1
Healthcare supranational	0.5	0.5	0	1
Healthcare international	0.8	0.4	0	1
Healthcare global	0.9	0.3	0	1
Healthcare world	0.7	0.5	0	1
Healthcare universal	0.6	0.5	0	

<211> 433

<213> Homo Sapien

Met Pro Gly Thr Tyr Ala Pro Ser Thr Thr Leu Ser Ser Pro Ser
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Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe
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Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
35 40 45

Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser
50 55 60

Tyr Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val Gly
65 70 75

Ala Gln Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg
80 85 90

Asp Ala Leu Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg
95 100 105

Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys
110 115 120

Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu
125 130 135

Gly Gly His Ser Leu Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe
140 145 150

Tyr Met Leu Gly Val Arg Tyr Leu Thr Leu Thr His Thr Cys Asn
155 160 165

Thr Pro Trp Ala Glu Ser Ser Ala Lys Gly Val His Ser Phe Tyr
170 175 180

Asn Asn Ile Ser Gly Leu Thr Asp Phe Gly Glu Lys Val Val Ala	185	190	195
Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser	200	205	210
Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val	215	220	225
Ile Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg	230	235	240
Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly	245	250	255
Val Val Met Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro	260	265	270
Ser Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Lys	275	280	285
Ala Val Ile Gly Ser Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp	290	295	300
Gly Ala Gly Lys Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr	305	310	315
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu	320	325	330
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg	335	340	345
Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu	350	355	360
Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser	365	370	375
Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln	380	385	390
Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala	395	400	405
Lys Trp Ser Val Ser Glu Ser Ser Pro His Met Ala Pro Val Leu	410	415	420
Ala Val Val Ala Thr Phe Pro Val Leu Ile Leu Trp Leu	425	430	

<210> 25

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<400> 25
agttctggtc agcctatgtg cc 22

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
cgtgatggcg tctttgtcca tggg 24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
ctccaccaat cccgatgaac ttgg 24

<210> 28
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 28
gagcagattg acctcatagc cgcgatgtgt gcctcctatt ctgagctgga 50

<210> 29
<211> 1416
<212> DNA
<213> Homo Sapien

<400> 29
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gatccgcggc cggaattct aaaccaacat gccgggcacc tacgctccct 100
cgaccacact cagtagtccc agcaccagg gcctgcaaga gcaggcacgg 150
gcctgatgc gggacttccc gctcgtggac ggccacaacg acctgcccct 200
ggtcctaagg caggtttacc agaaagggct acaggatggt aacctgcgca 250
atttcagcta cggccagacc agcctggaca ggcttagaga tggcctcgtg 300
ggcgcccagt tctggtcagc ctatgtgcca tgccagaccc aggaccggga 350
tgccctgcgc ctcaccctgg agcagattga cctcatagc cgcgatgtgtg 400

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cctcctattc tgagctggag cttgtgacct cggctaaagc tctgaacgac 450
actcagaaat tggcctgcct catcgggtgta gaggggtggcc actcgtctgga 500
caatagcctc tccatcttac gtaccttcta catgctggga gtgcgctacc 550
tgacgctcac ccacacctgc aacacacctc gggcagagag ctccgctaag 600
ggcgctccact ccttctacaa caacatcagc gggctgactg actttggtga 650
gaagggtggtg gcagaaatga accgcctggg catgatggta gacttatccc 700
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gttcacggg attggtggag attatgatgg ggcgggcaaa ttccctcagg 1000
ggctggaaga cgtgtccaca taccgggtcc tgatagagga gttgctgagt 1050
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actcactgag attcccatac actggacagc caagttacca gccaaagtgt 1300
cagtctcaga gtctctcccc caccctgaca aaactcacac atgcccaccg 1350
tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc 1400
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<210> 30

<211> 446

<212> PRT

<213> Homo Sapien

<400> 30

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Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe
20 25 30

Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
35 40 45

Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser

	50		55		60
Tyr Gly Gln Thr Ser	Leu Asp Arg Leu Arg Asp Gly Leu Val Gly				
	65		70		75
Ala Gln Phe Trp Ser	Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg				
	80		85		90
Asp Ala Leu Arg Leu	Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg				
	95		100		105
Met Cys Ala Ser Tyr	Ser Glu Leu Glu Leu Val Thr Ser Ala Lys				
	110		115		120
Ala Leu Asn Asp Thr	Gln Lys Leu Ala Cys Leu Ile Gly Val Glu				
	125		130		135
Gly Gly His Ser Leu	Asp Asn Ser Leu Ser Ile Leu Arg Thr Phe				
	140		145		150
Tyr Met Leu Gly Val	Arg Tyr Leu Thr Leu Thr His Thr Cys Asn				
	155		160		165
Thr Pro Trp Ala Glu	Ser Ser Ala Lys Gly Val His Ser Phe Tyr				
	170		175		180
Asn Asn Ile Ser Gly	Leu Thr Asp Phe Gly Glu Lys Val Val Ala				
	185		190		195
Glu Met Asn Arg Leu	Gly Met Met Val Asp Leu Ser His Val Ser				
	200		205		210
Asp Ala Val Ala Arg	Arg Ala Leu Glu Val Ser Gln Ala Pro Val				
	215		220		225
Ile Phe Ser His Ser	Ala Ala Arg Gly Val Cys Asn Ser Ala Arg				
	230		235		240
Asn Val Pro Asp Asp	Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly				
	245		250		255
Val Val Met Val Ser	Leu Ser Met Gly Val Ile Gln Cys Asn Pro				
	260		265		270
Ser Ala Asn Val Ser	Thr Val Ala Asp His Phe Asp His Ile Lys				
	275		280		285
Ala Val Ile Gly Ser	Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp				
	290		295		300
Gly Ala Gly Lys Phe	Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr				
	305		310		315
Pro Val Leu Ile Glu	Glu Leu Leu Ser Arg Gly Trp Ser Glu Glu				
	320		325		330
Glu Leu Gln Gly Val	Leu Arg Gly Asn Leu Leu Arg Val Phe Arg				
	335		340		345

Gln Val Glu Lys Val Gln Glu Glu Asn Lys Trp Gln Ser Pro Leu
 350 355 360
 Glu Asp Lys Phe Pro Asp Glu Gln Leu Ser Ser Ser Cys His Ser
 365 370 375
 Asp Leu Ser Arg Leu Arg Gln Arg Gln Ser Leu Thr Ser Gly Gln
 380 385 390
 Glu Leu Thr Glu Ile Pro Ile His Trp Thr Ala Lys Leu Pro Ala
 395 400 405
 Lys Trp Ser Val Ser Glu Ser Ser Pro His Pro Asp Lys Thr His
 410 415 420
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 425 430 435
 Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 440 445

<210> 31
 <211> 1790
 <212> DNA
 <213> Homo Sapien

<400> 31
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 gcgtcccgcg ccctgcgcca ccgcgcgcca gccgcagccc gccgcgcgcc 100
 cccggcagcg ccggccccat gccgcgcggc cgccgggggc ccgcgcgcca 150
 atccgcgcgg cggcgcgcgc cgttgctgcc cctgctgctg ctgctctgcg 200
 tctcgggggc gccgcgagcc ggatcaggag cccacacagc tgtgatcagt 250
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Ala Pro Arg Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro  
          35                40                      45  
  
Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys  
          50                55                      60
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Ser Val His Gly Asp	Pro Pro Gly Ala Thr Ala Glu Gly Leu Tyr	65	70	75
Trp Thr Leu Asn Gly Arg Arg Leu Pro	Pro Glu Leu Ser Arg Val	80	85	90
Leu Asn Ala Ser Thr Leu Ala Leu Ala	Leu Ala Asn Leu Asn Gly	95	100	105
Ser Arg Gln Arg Ser Gly Asp Asn Leu	Val Cys His Ala Arg Asp	110	115	120
Gly Ser Ile Leu Ala Gly Ser Cys Leu	Tyr Val Gly Leu Pro Pro	125	130	135
Glu Lys Pro Val Asn Ile Ser Cys Trp	Ser Lys Asn Met Lys Asp	140	145	150
Leu Thr Cys Arg Trp Thr Pro Gly Ala	His Gly Glu Thr Phe Leu	155	160	165
His Thr Asn Tyr Ser Leu Lys Tyr Lys	Leu Arg Trp Tyr Gly Gln	170	175	180
Asp Asn Thr Cys Glu Glu Tyr His Thr	Val Gly Pro His Ser Cys	185	190	195
His Ile Pro Lys Asp Leu Ala Leu Phe	Thr Pro Tyr Glu Ile Trp	200	205	210
Val Glu Ala Thr Asn Arg Leu Gly Ser	Ala Arg Ser Asp Val Leu	215	220	225
Thr Leu Asp Ile Leu Asp Val Val Thr	Thr Asp Pro Pro Pro Asp	230	235	240
Val His Val Ser Arg Val Gly Gly Leu	Glu Asp Gln Leu Ser Val	245	250	255
Arg Trp Val Ser Pro Pro Ala Leu Lys	Asp Phe Leu Phe Gln Ala	260	265	270
Lys Tyr Gln Ile Arg Tyr Arg Val Glu	Asp Ser Val Asp Trp Lys	275	280	285
Val Val Asp Asp Val Ser Asn Gln Thr	Ser Cys Arg Leu Ala Gly	290	295	300
Leu Lys Pro Gly Thr Val Tyr Phe Val	Gln Val Arg Cys Asn Pro	305	310	315
Phe Gly Ile Tyr Gly Ser Lys Lys Ala	Gly Ile Trp Ser Glu Trp	320	325	330
Ser His Pro Thr Ala Ala Ser Thr Pro	Arg Ser Glu Arg Pro Gly	335	340	345
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Parameter	Value
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Initial population sex	1000
Initial population weight	1000
Initial population length	1000
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Initial population volume	1000
Initial population mass	1000
Initial population energy	1000
Initial population momentum	1000
Initial population force	1000
Initial population pressure	1000
Initial population temperature	1000
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Initial population wind speed	1000
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Initial population soil moisture	1000
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Initial population land use	1000
Initial population climate	1000
Initial population environment	1000
Initial population society	1000
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Initial population religion	1000
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Initial population basketball court	1000
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項目	単位	数値
1. 総人口	人	1,234,567
2. 男性人口	人	612,345
3. 女性人口	人	622,222
4. 人口密度	人/平方キロメートル	123.45
5. 出生率	‰	10.5
6. 死亡率	‰	8.2
7. 自然増減率	‰	2.3
8. 平均寿命	歳	75.6
9. 識字率	%	98.7
10. 労働力人口	人	567,890
11. 失業率	%	4.5
12. 所得総額	億円	1,500.0
13. 消費税率	%	10.0
14. 財政赤字	億円	500.0
15. 外債総額	億円	1,000.0
16. 貿易収支	億円	200.0
17. 観光収入	億円	300.0
18. 教育費	億円	150.0
19. 医療費	億円	120.0
20. 社会保障費	億円	80.0
21. 環境費	億円	60.0
22. 防衛費	億円	40.0
23. 文化費	億円	30.0
24. 交通費	億円	20.0
25. 住宅費	億円	10.0
26. 福祉費	億円	5.0
27. 防災費	億円	3.0
28. 国際協力費	億円	2.0
29. 研究開発費	億円	1.0
30. 情報通信費	億円	0.5
31. 環境整備費	億円	0.2
32. 行政費	億円	0.1
33. 災害復旧費	億円	0.05
34. 文化振興費	億円	0.02
35. 交通整備費	億円	0.01
36. 住宅整備費	億円	0.005
37. 福祉整備費	億円	0.002
38. 防災整備費	億円	0.001
39. 国際交流費	億円	0.0005
40. 研究開発費	億円	0.0002
41. 情報通信費	億円	0.0001
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44. 災害復旧費	億円	0.00001
45. 文化振興費	億円	0.000005
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47. 住宅整備費	億円	0.000001
48. 福祉整備費	億円	0.0000005
49. 防災整備費	億円	0.0000002
50. 国際交流費	億円	0.0000001
51. 研究開発費	億円	0.00000005
52. 情報通信費	億円	0.00000002
53. 環境整備費	億円	0.00000001
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55. 災害復旧費	億円	0.000000002
56. 文化振興費	億円	0.000000001
57. 交通整備費	億円	0.0000000005
58. 住宅整備費	億円	0.0000000002
59. 福祉整備費	億円	0.0000000001
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81. 福祉整備費	億円	0.000000000000000005
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89. 文化振興費	億円	0.00000000000000000001
90. 交通整備費	億円	0.000000000000000000005
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<213> Homo Sapien

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Arg Lys Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly
35 40 45

His Gly Ile Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys
50 55 60

Ser Lys Leu Val Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu
65 70 75

Thr Ala Ala Lys Cys Lys Gly Leu Gly Ala Lys Val His Thr Phe
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Val Val Asp Cys Ser Asn Arg Glu Asp Ile Tyr Ser Ser Ala Lys
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Lys Val Lys Ala Glu Ile Gly Asp Val Ser Ile Leu Val Asn Asn
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Ala Gly Val Val Tyr Thr Ser Asp Leu Phe Ala Thr Gln Asp Pro
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Gln Ile Glu Lys Thr Phe Glu Val Asn Val Leu Ala His Phe Trp
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Thr Thr Lys Ala Phe Leu Pro Ala Met Thr Lys Asn Asn His Gly
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His Ile Val Thr Val Ala Ser Ala Ala Gly His Val Ser Val Pro
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Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe
185 190 195

32

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	15.2	5.8	10	25
Health status	0.7	0.4	0	1
Stress level	3.2	1.1	1	5
Life satisfaction	4.1	0.8	3	5
Work engagement	3.8	0.9	2	5
Organizational commitment	4.2	0.7	3	5
Job satisfaction	4.0	0.8	3	5
Turnover intention	1.5	0.6	1	3
Organizational citizenship behavior	3.5	0.9	2	5
Employee well-being	3.9	0.8	2	5
Work-life balance	3.7	0.9	2	5
Job design	3.6	0.8	2	5
Supervisor support	3.8	0.7	2	5
Team cohesion	3.9	0.8	2	5
Organizational culture	3.7	0.9	2	5
Leadership style	3.8	0.7	2	5
Employee engagement	3.9	0.8	2	5
Organizational performance	3.8	0.9	2	5
Customer satisfaction	3.7	0.8	2	5
Employee retention	3.9	0.7	2	5
Organizational innovation	3.8	0.9	2	5
Employee productivity	3.9	0.8	2	5
Organizational flexibility	3.7	0.9	2	5
Employee loyalty	3.8	0.7	2	5
Organizational reputation	3.9	0.8	2	5
Employee turnover	3.7	0.9	2	5
Organizational success	3.8	0.7	2	5
Employee commitment	3.9	0.8	2	5
Organizational effectiveness	3.8	0.9	2	5
Employee satisfaction	3.9	0.7	2	5
Organizational climate	3.7	0.8	2	5
Employee motivation	3.8	0.9	2	5
Organizational strategy	3.9	0.7	2	5
Employee performance	3.8	0.8	2	5
Organizational growth	3.7	0.9	2	5
Employee well-being	3.9	0.7	2	5
Organizational success	3.8	0.8	2	5
Employee commitment	3.9	0.9	2	5
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Employee satisfaction	3.8	0.8	2	5
Organizational climate	3.9	0.9	2	5
Employee motivation	3.7	0.7	2	5
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Organizational growth	3.7	0.9	2	5
Employee well-being	3.8	0.8	2	5
Organizational success	3.9	0.7	2	5
Employee commitment	3.7	0.9	2	5
Organizational effectiveness	3.8	0.8	2	5
Employee satisfaction	3.9	0.7	2	5
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Organizational climate	3.9	0.7	2	5
Employee motivation	3.7	0.9	2	5
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Employee performance	3.9	0.7	2	5
Organizational growth	3.7	0.9	2	5
Employee well-being	3.8	0.8	2	5
Organizational success	3.9	0.7	2	5
Employee commitment	3.7	0.9	2	5
Organizational effectiveness	3.8	0.8	2	5
Employee satisfaction	3.9	0.7	2	5
Organizational climate	3.7	0.9	2	

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 <213> Homo Sapien

<400> 42

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His	Pro	Gly	Leu	Pro	Gly	Thr	Pro	Gly	His	His	Gly	Ser	Gln	Gly	35	40	45	
Leu	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Ala	Pro	Gly	50	55	60	
Ala	Pro	Gly	Glu	Lys	Gly	Glu	Gly	Gly	Arg	Pro	Gly	Leu	Pro	Gly	65	70	75	
Pro	Arg	Gly	Asp	Pro	Gly	Pro	Arg	Gly	Glu	Ala	Gly	Pro	Ala	Gly	80	85	90	
Pro	Thr	Gly	Pro	Ala	Gly	Glu	Cys	Ser	Val	Pro	Pro	Arg	Ser	Ala	95	100	105	
Phe	Ser	Ala	Lys	Arg	Ser	Glu	Ser	Arg	Val	Pro	Pro	Pro	Ser	Asp	110	115	120	
Ala	Pro	Leu	Pro	Phe	Asp	Arg	Val	Leu	Val	Asn	Glu	Gln	Gly	His	125	130	135	
Tyr	Asp	Ala	Val	Thr	Gly	Lys	Phe	Thr	Cys	Gln	Val	Pro	Gly	Val	140	145	150	
Tyr	Tyr	Phe	Ala	Val	His	Ala	Thr	Val	Tyr	Arg	Ala	Ser	Leu	Gln	155	160	165	
Phe	Asp	Leu	Val	Lys	Asn	Gly	Glu	Ser	Ile	Ala	Ser	Phe	Phe	Gln	170	175	180	
Phe	Phe	Gly	Gly	Trp	Pro	Lys	Pro	Ala	Ser	Leu	Ser	Gly	Gly	Ala	185	190	195	
Met	Val	Arg	Leu	Glu	Pro	Glu	Asp	Gln	Val	Trp	Val	Gln	Val	Gly	200	205	210	
Val	Gly	Asp	Tyr	Ile	Gly	Ile	Tyr	Ala	Ser	Ile	Lys	Thr	Asp	Ser	215	220	225	
Thr	Phe	Ser	Gly	Phe	Leu	Val	Tyr	Ser	Asp	Trp	His	Ser	Ser	Pro	230	235	240	
Val	Phe	Ala																

<210> 43
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
tacaggccca gtcaggacca gggg 24

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 44
agccagcctc gctctcgg 18

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 45
gtctgcatc aggtctgg 18

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 46
gaaagaggca atggattcgc 20

<210> 47
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
gacttacact tgccagcaca gcac 24

<210> 48
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 48

ggagcaccac caactggagg gtccggagta gcgagcgccc cgaag 45

<210> 49

<211> 1876

<212> DNA

<213> Homo Sapien

<400> 49

ctcttttgtc caccagccca gctgactcc tggagattgt gaatagctcc 50
atccagcctg agaaacaagc cgggtggctg agccaggctg tgcacggagc 100
acctgacggg cccaacagac ccattgctga tccagagacc tcccctggcc 150
gggggcatct cctggctgtg ctctggccc tcttggcac cacctgggca 200
gaggtgtggc cccccagct gcaggagcag gctccgatgg ccggagccct 250
gaacaggaag gagagtttct tgctcctctc cctgcacaac cgctgcgca 300
gctgggtcca gcccctgcg gctgacatgc ggaggctgga ctggagtga 350
agctggccc aactggctca agccaggga gccctctgtg gaatcccaac 400
cccgagcctg gcattcgcc tgtggcgcc cctgcaagt ggctggaaca 450
tgcagctgct gcccgcgggc ttggcgctct ttgttgaagt ggtcagccta 500
tggtttgcag aggggcagcg gtacagccac gcggcaggag agtgtgctcg 550
caacgccacc tgcaccact acacgcagct cgtgtgggcc acctcaagcc 600
agctgggctg tgggcggcac ctgtgctctg caggccagac agcgatagaa 650
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gtgtctcagg ctgcttcaaa gcctgggacc atgcaggggg gctctgtgag 800
gtccccagga atccttgtcg catgagctgc cagaacctg gacgtctcaa 850
catcagcacc tgccactgcc actgtcccc tggctacacg ggcagatact 900
gccaagtga gtgcagcctg cagtgtgtgc acggccggtt ccgggaggag 950
gagtgtcgt gcgtctgtga catcggtac gggggagccc agtgtgccac 1000
caagggtgat tttcccttcc acacctgtga cctgaggatc gacggagact 1050
gcttcatggt gtcttcagag gcagacacct attacagagc caggatgaaa 1100
tgtcagagga aaggcggggg gctggcccag atcaagagcc agaaagtga 1150

ggacatcctc gccttctatc tgggccgcct ggagaccacc aacgaggtga 1200
 ctgacagtga ctctgagacc aggaacttct ggatcgggct cacctacaag 1250
 accgccaagg actccttccg ctgggccaca ggggagcacc aggccttcac 1300
 cagttttgcc tttgggcagc ctgacaacca cgggctgggtg tggctgagtg 1350
 ctgccatggg gtttggcaac tgcgtggagc tgcaggcttc agctgccttc 1400
 aactggaacg accagcgctg caaaacccga aaccgttaca tctgccagtt 1450
 tgcccaggag cacatctccc ggtggggccc agggctcctga ggcctgacca 1500
 catggetccc tgcctgccc tgggagcacc ggctctgctt acctgtctgc 1550
 ccacctgtct ggaacaaggg ccagggttaag accacatgcc tcatgtccaa 1600
 agaggtctca gaccttgac aatgccagaa gttgggcaga gagaggcagg 1650
 gagggcagtg agggccaggg agtgagtgtt agaagaagct ggggcccttc 1700
 gcctgctttt gattgggaag atgggcttca attagatggc gaaggagagg 1750
 acaccgccag tgggtcaaaa aggtgctct cttccacctg gccagaccc 1800
 tgtggggcag cggagcttcc ctgtggcatg aacccacgg ggtattaaat 1850
 tatgaatcag ctgaaaaaaaa aaaaaa 1876

<210> 50
 <211> 455
 <212> PRT
 <213> Homo Sapien

<400> 50
 Met Leu His Pro Glu Thr Ser Pro Gly Arg Gly His Leu Leu Ala
 1 5 10 15
 Val Leu Leu Ala Leu Leu Gly Thr Thr Trp Ala Glu Val Trp Pro
 20 25 30
 Pro Gln Leu Gln Glu Gln Ala Pro Met Ala Gly Ala Leu Asn Arg
 35 40 45
 Lys Glu Ser Phe Leu Leu Leu Ser Leu His Asn Arg Leu Arg Ser
 50 55 60
 Trp Val Gln Pro Pro Ala Ala Asp Met Arg Arg Leu Asp Trp Ser
 65 70 75
 Asp Ser Leu Ala Gln Leu Ala Gln Ala Arg Ala Ala Leu Cys Gly
 80 85 90
 Ile Pro Thr Pro Ser Leu Ala Ser Gly Leu Trp Arg Thr Leu Gln
 95 100 105
 Val Gly Trp Asn Met Gln Leu Leu Pro Ala Gly Leu Ala Ser Phe

					110						115						120
Val	Glu	Val	Val	Ser	Leu	Trp	Phe	Ala	Glu	Gly	Gln	Arg	Tyr	Ser			
				125					130					135			
His	Ala	Ala	Gly	Glu	Cys	Ala	Arg	Asn	Ala	Thr	Cys	Thr	His	Tyr			
				140					145					150			
Thr	Gln	Leu	Val	Trp	Ala	Thr	Ser	Ser	Gln	Leu	Gly	Cys	Gly	Arg			
				155					160					165			
His	Leu	Cys	Ser	Ala	Gly	Gln	Thr	Ala	Ile	Glu	Ala	Phe	Val	Cys			
				170					175					180			
Ala	Tyr	Ser	Pro	Gly	Gly	Asn	Trp	Glu	Val	Asn	Gly	Lys	Thr	Ile			
				185					190					195			
Ile	Pro	Tyr	Lys	Lys	Gly	Ala	Trp	Cys	Ser	Leu	Cys	Thr	Ala	Ser			
				200					205					210			
Val	Ser	Gly	Cys	Phe	Lys	Ala	Trp	Asp	His	Ala	Gly	Gly	Leu	Cys			
				215					220					225			
Glu	Val	Pro	Arg	Asn	Pro	Cys	Arg	Met	Ser	Cys	Gln	Asn	His	Gly			
				230					235					240			
Arg	Leu	Asn	Ile	Ser	Thr	Cys	His	Cys	His	Cys	Pro	Pro	Gly	Tyr			
				245					250					255			
Thr	Gly	Arg	Tyr	Cys	Gln	Val	Arg	Cys	Ser	Leu	Gln	Cys	Val	His			
				260					265					270			
Gly	Arg	Phe	Arg	Glu	Glu	Glu	Cys	Ser	Cys	Val	Cys	Asp	Ile	Gly			
				275					280					285			
Tyr	Gly	Gly	Ala	Gln	Cys	Ala	Thr	Lys	Val	His	Phe	Pro	Phe	His			
				290					295					300			
Thr	Cys	Asp	Leu	Arg	Ile	Asp	Gly	Asp	Cys	Phe	Met	Val	Ser	Ser			
				305					310					315			
Glu	Ala	Asp	Thr	Tyr	Tyr	Arg	Ala	Arg	Met	Lys	Cys	Gln	Arg	Lys			
				320					325					330			
Gly	Gly	Val	Leu	Ala	Gln	Ile	Lys	Ser	Gln	Lys	Val	Gln	Asp	Ile			
				335					340					345			
Leu	Ala	Phe	Tyr	Leu	Gly	Arg	Leu	Glu	Thr	Thr	Asn	Glu	Val	Thr			
				350					355					360			
Asp	Ser	Asp	Phe	Glu	Thr	Arg	Asn	Phe	Trp	Ile	Gly	Leu	Thr	Tyr			
				365					370					375			
Lys	Thr	Ala	Lys	Asp	Ser	Phe	Arg	Trp	Ala	Thr	Gly	Glu	His	Gln			
				380					385					390			
Ala	Phe	Thr	Ser	Phe	Ala	Phe	Gly	Gln	Pro	Asp	Asn	His	Gly	Leu			
				395					400					405			

Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu
410 415 420

Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr
425 430 435

Arg Asn Arg Tyr Ile Cys Gln Phe Ala Gln Glu His Ile Ser Arg
440 445 450

Trp Gly Pro Gly Ser
455

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 51
aggaacttct ggatcgggct cacc 24

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 52
gggtctgggc caggtggaag agag 24

<210> 53
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
gccaaggact ccttccgctg ggccacaggg gagcaccagg ccttc 45

<210> 54
<211> 2331
<212> DNA
<213> Homo Sapien

<400> 54
cggacgcgtg ggctgggcgc tgcaaagcgt gtccgcgcgg gtccccgagc 50
gtccgcgcc ctcgccccgc catgctcctg ctgctggggc tgtgcctggg 100
gctgtccctg tgtgtggggg cgcaggaaga ggccgagagc tggggccact 150
cttcggagca ggatggactc aggggtcccga ggcaagtcag actgttgag 200

aggctgaaaa	ccaaaccttt	gatgacagaa	ttctcagtga	agctctacat	250
catttcccg	tatgccttca	ctacggtttc	ctgcagaatg	ctgaacagag	300
cttctgaaga	ccaggacatt	gagttccaga	tgcagattcc	agctgcagct	350
ttcatcacca	acttcactat	gcttattgga	gacaagggtg	atcagggcga	400
aattacagag	agagaaaaga	agagtgggtga	tagggtaaaa	gagaaaagga	450
ataaaaccac	agaagaaaat	ggagagaagg	ggactgaaat	attcagagct	500
tctgcagtga	ttcccagcaa	ggacaaagcc	gcctttttcc	tgagttatga	550
ggagcttctg	cagagggcgc	tgggcaagta	cgagcacagc	atcagcgtgc	600
ggccccagca	gctgtccggg	aggctgagcg	tggacgtgaa	tatcctggag	650
agcgcgggca	tgcataccct	ggaggtgctg	ccgcttcaca	acagcaggca	700
gaggggcagt	gggcgcgggg	aagatgattc	tgggcctccc	ccatctactg	750
tcattaacca	aatgaaaca	tttgccaaca	taatttttaa	acctactgta	800
gtacaacaag	ccaggattgc	ccagaatgga	attttgggag	actttatcat	850
tagatatgac	gtcaatagag	aacagagcat	tggggacatc	caggttctaa	900
atggctattt	tgtgcactac	tttgctccta	aagaccttcc	tcctttaccc	950
aagaatgtgg	tattcgtgct	tgacagcagt	gcttctatgg	tgggaaccaa	1000
actccggcag	accaagggat	ccctcttcac	aattctccat	gacctccgac	1050
cccaggaccg	tttcagtatc	attggatttt	ccaaccggat	caaagtatgg	1100
aaggaccact	tgatatcagt	cactccagac	agcatcaggg	atgggaaagt	1150
gtacattcac	catatgtcac	ccactggagg	cacagacatc	aacggggccc	1200
tgcagagggc	catcaggctc	ctcaacaagt	acgtggccca	cagtggcatt	1250
ggagaccgga	gcgtgtccct	catcgtcttc	ctgacgggat	ggaagcccac	1300
ggtcggggag	acgcacaccc	tcaagatcct	caacaacacc	cgagaggccg	1350
cccgaggcca	agtctgcata	ttcaccattg	gcatcggcaa	cgacgtggac	1400
ttcaggctgc	tggagaaact	gtcgtcggag	aactgtggcc	tcacacggcg	1450
cgtgcacgag	gaggaggacg	caggctcgca	gctcatcggg	ttctacgatg	1500
aaatcaggac	cccgtcctc	tctgacatcc	gcatcgatta	ccccccagc	1550
tcagtgggtg	aggccaccaa	gacctgttc	cccaactact	tcaacggctc	1600
ggagatcatc	attgcgggga	agctgggtgga	caggaagctg	gatcacctgc	1650

Arg Val Lys Glu Lys Arg Asn Lys Thr Thr Glu Glu Asn Gly Glu	125	130	135
Lys Gly Thr Glu Ile Phe Arg Ala Ser Ala Val Ile Pro Ser Lys	140	145	150
Asp Lys Ala Ala Phe Phe Leu Ser Tyr Glu Glu Leu Leu Gln Arg	155	160	165
Arg Leu Gly Lys Tyr Glu His Ser Ile Ser Val Arg Pro Gln Gln	170	175	180
Leu Ser Gly Arg Leu Ser Val Asp Val Asn Ile Leu Glu Ser Ala	185	190	195
Gly Ile Ala Ser Leu Glu Val Leu Pro Leu His Asn Ser Arg Gln	200	205	210
Arg Gly Ser Gly Arg Gly Glu Asp Asp Ser Gly Pro Pro Pro Ser	215	220	225
Thr Val Ile Asn Gln Asn Glu Thr Phe Ala Asn Ile Ile Phe Lys	230	235	240
Pro Thr Val Val Gln Gln Ala Arg Ile Ala Gln Asn Gly Ile Leu	245	250	255
Gly Asp Phe Ile Ile Arg Tyr Asp Val Asn Arg Glu Gln Ser Ile	260	265	270
Gly Asp Ile Gln Val Leu Asn Gly Tyr Phe Val His Tyr Phe Ala	275	280	285
Pro Lys Asp Leu Pro Pro Leu Pro Lys Asn Val Val Phe Val Leu	290	295	300
Asp Ser Ser Ala Ser Met Val Gly Thr Lys Leu Arg Gln Thr Lys	305	310	315
Asp Ala Leu Phe Thr Ile Leu His Asp Leu Arg Pro Gln Asp Arg	320	325	330
Phe Ser Ile Ile Gly Phe Ser Asn Arg Ile Lys Val Trp Lys Asp	335	340	345
His Leu Ile Ser Val Thr Pro Asp Ser Ile Arg Asp Gly Lys Val	350	355	360
Tyr Ile His His Met Ser Pro Thr Gly Gly Thr Asp Ile Asn Gly	365	370	375
Ala Leu Gln Arg Ala Ile Arg Leu Leu Asn Lys Tyr Val Ala His	380	385	390
Ser Gly Ile Gly Asp Arg Ser Val Ser Leu Ile Val Phe Leu Thr	395	400	405
Asp Gly Lys Pro Thr Val Gly Glu Thr His Thr Leu Lys Ile Leu			

410										415					420				
Asn	Asn	Thr	Arg	Glu	Ala	Ala	Arg	Gly	Gln	Val	Cys	Ile	Phe	Thr					
				425					430					435					
Ile	Gly	Ile	Gly	Asn	Asp	Val	Asp	Phe	Arg	Leu	Leu	Glu	Lys	Leu					
				440					445					450					
Ser	Leu	Glu	Asn	Cys	Gly	Leu	Thr	Arg	Arg	Val	His	Glu	Glu	Glu					
				455					460					465					
Asp	Ala	Gly	Ser	Gln	Leu	Ile	Gly	Phe	Tyr	Asp	Glu	Ile	Arg	Thr					
				470					475					480					
Pro	Leu	Leu	Ser	Asp	Ile	Arg	Ile	Asp	Tyr	Pro	Pro	Ser	Ser	Val					
				485					490					495					
Val	Gln	Ala	Thr	Lys	Thr	Leu	Phe	Pro	Asn	Tyr	Phe	Asn	Gly	Ser					
				500					505					510					
Glu	Ile	Ile	Ile	Ala	Gly	Lys	Leu	Val	Asp	Arg	Lys	Leu	Asp	His					
				515					520					525					
Leu	His	Val	Glu	Val	Thr	Ala	Ser	Asn	Ser	Lys	Lys	Phe	Ile	Ile					
				530					535					540					
Leu	Lys	Thr	Asp	Val	Pro	Val	Arg	Pro	Gln	Lys	Ala	Gly	Lys	Asp					
				545					550					555					
Val	Thr	Gly	Ser	Pro	Arg	Pro	Gly	Gly	Asp	Gly	Glu	Gly	Asp	Thr					
				560					565					570					
Asn	His	Ile	Glu	Arg	Leu	Trp	Ser	Tyr	Leu	Thr	Thr	Lys	Glu	Leu					
				575					580					585					
Leu	Ser	Ser	Trp	Leu	Gln	Ser	Asp	Asp	Glu	Pro	Glu	Lys	Glu	Arg					
				590					595					600					
Leu	Arg	Gln	Arg	Ala	Gln	Ala	Leu	Ala	Val	Ser	Tyr	Arg	Phe	Leu					
				605					610					615					
Thr	Pro	Phe	Thr	Ser	Met	Lys	Leu	Arg	Gly	Pro	Val	Pro	Arg	Met					
				620					625					630					
Asp	Gly	Leu	Glu	Glu	Ala	His	Gly	Met	Ser	Ala	Ala	Met	Gly	Pro					
				635					640					645					
Glu	Pro	Val	Val	Gln	Ser	Val	Arg	Gly	Ala	Gly	Thr	Gln	Pro	Gly					
				650					655					660					
Pro	Leu	Leu	Lys	Lys	Pro	Asn	Ser	Val	Lys	Lys	Lys	Gln	Asn	Lys					
				665					670					675					
Thr	Lys	Lys	Arg	His	Gly	Arg	Asp	Gly	Val	Phe	Pro	Leu	His	His					
				680					685					690					
Leu	Gly	Ile	Arg																

<210> 56
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 56
 gtgggaacca aactccggca gacc 24

<210> 57
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 57
 cacatcgagc gtctctgg 18

<210> 58
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 58
 agccgctcct tctccggttc atcg 24

<210> 59
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 59
 tggaaggacc acttgatata agtcaactcca gacagcatca gggatggg 48

<210> 60
 <211> 1413
 <212> DNA
 <213> Homo Sapien

<400> 60
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 ccagtgtgcg gcggcagcgg cggcgggggc gcctcccggg ctccggcttc 100
 tgctgttgct cttctccgcc gcggcactga tccccacagg tgatgggcag 150
 aatctgttta cgaaagacgt gacagtgate gagggagagg ttgcgaccat 200

cagttgccaa gtcaataaga gtgacgactc tgtgattcag ctactgaatc 250
ccaacaggca gaccatztat ttcagggact tcaggccttt gaaggacagc 300
aggtttcagt tgctgaatzt ttctagcagt gaactcaaag tatcattgac 350
aaacgtctca attttctgatg aaggaagata cttttgccag ctctataaccg 400
atcccccaaca ggaaagttac accaccatca cagtccctggc cccaccacgt 450
aatctgatga tcgatatacca gaaagacact gcgggtggaag gtgaggagat 500
tgaagtcaac tgcactgcta tggccagcaa gccagccacg actatcaggt 550
ggttcaaagg gaacacagag ctaaaaggca aatcggaggt ggaagagtgg 600
tcagacatgt aactgtgac cagtcagctg atgctgaagg tgcacaagga 650
ggacgatggg gtcccagtga tctgccaggc ggagcaccct gcgggtcactg 700
gaaacctgca gaccagcgg tatctagaag tacagtataa gcctcaagtg 750
cacattcaga tgacttatcc tctacaaggc ttaaccggg aaggggacgc 800
gcttgagtta acatgtgaag ccacgggaa gccccagcct gtgatggtaa 850
cttgggtgag agtcgatgat gaaatgcctc aacacgcct actgtctggg 900
cccaacctgt tcatcaataa cctaaacaaa acagataatg gtacataaccg 950
ctgtgaagct tcaaacatag tggggaaagc tcaactggat tatatgctgt 1000
atgtatacga tcccccaaca actatccctc ctcccacaac aaccaccacc 1050
accaccacca ccaccaccac caccatcctt accatcatca cagattccccg 1100
agcaggtgaa gaaggctcga tcagggcagt ggatcatgcc gtgatcgggtg 1150
gcgtcgtggc ggtggtggtg ttcgccatgc tgtgcttgc catcattctg 1200
gggcgctatt ttgccagaca taaaggatca tacttcactc atgaagccaa 1250
aggagccgat gacgcagcag acgcagacac agctataatc aatgcagaag 1300
gaggacagaa caactccgaa gaaaagaaa agtacttcat ctagatcagc 1350
ctttttgttt caatgaggtg tccaactggc cctattttaga tgataaagag 1400
acagtgatat tgg 1413

<210> 61
<211> 440
<212> PRT
<213> Homo Sapien

<400> 61
Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala
1 5 10 15

Ala	Ala	Ala	Ala	Ala 20	Pro	Pro	Gly	Leu	Arg 25	Leu	Leu	Leu	Leu	Leu 30
Phe	Ser	Ala	Ala	Ala 35	Leu	Ile	Pro	Thr	Gly 40	Asp	Gly	Gln	Asn	Leu 45
Phe	Thr	Lys	Asp	Val 50	Thr	Val	Ile	Glu	Gly 55	Glu	Val	Ala	Thr	Ile 60
Ser	Cys	Gln	Val	Asn 65	Lys	Ser	Asp	Asp	Ser 70	Val	Ile	Gln	Leu	Leu 75
Asn	Pro	Asn	Arg	Gln 80	Thr	Ile	Tyr	Phe	Arg 85	Asp	Phe	Arg	Pro	Leu 90
Lys	Asp	Ser	Arg	Phe 95	Gln	Leu	Leu	Asn	Phe 100	Ser	Ser	Ser	Glu	Leu 105
Lys	Val	Ser	Leu	Thr 110	Asn	Val	Ser	Ile	Ser 115	Asp	Glu	Gly	Arg	Tyr 120
Phe	Cys	Gln	Leu	Tyr 125	Thr	Asp	Pro	Pro	Gln 130	Glu	Ser	Tyr	Thr	Thr 135
Ile	Thr	Val	Leu	Val 140	Pro	Pro	Arg	Asn	Leu 145	Met	Ile	Asp	Ile	Gln 150
Lys	Asp	Thr	Ala	Val 155	Glu	Gly	Glu	Glu	Ile 160	Glu	Val	Asn	Cys	Thr 165
Ala	Met	Ala	Ser	Lys 170	Pro	Ala	Thr	Thr	Ile 175	Arg	Trp	Phe	Lys	Gly 180
Asn	Thr	Glu	Leu	Lys 185	Gly	Lys	Ser	Glu	Val 190	Glu	Glu	Trp	Ser	Asp 195
Met	Tyr	Thr	Val	Thr 200	Ser	Gln	Leu	Met	Leu 205	Lys	Val	His	Lys	Glu 210
Asp	Asp	Gly	Val	Pro 215	Val	Ile	Cys	Gln	Val 220	Glu	His	Pro	Ala	Val 225
Thr	Gly	Asn	Leu	Gln 230	Thr	Gln	Arg	Tyr	Leu 235	Glu	Val	Gln	Tyr	Lys 240
Pro	Gln	Val	His	Ile 245	Gln	Met	Thr	Tyr	Pro 250	Leu	Gln	Gly	Leu	Thr 255
Arg	Glu	Gly	Asp	Ala 260	Leu	Glu	Leu	Thr	Cys 265	Glu	Ala	Ile	Gly	Lys 270
Pro	Gln	Pro	Val	Met 275	Val	Thr	Trp	Val	Arg 280	Val	Asp	Asp	Glu	Met 285
Pro	Gln	His	Ala	Val 290	Leu	Ser	Gly	Pro	Asn 295	Leu	Phe	Ile	Asn	Asn 300
Leu	Asn	Lys	Thr	Asp	Asn	Gly	Thr	Tyr	Arg	Cys	Glu	Ala	Ser	Asn

<400> 64
atcatcacag attcccgagc 20

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
ttcaatctcc tcaccttcca ccgc 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
atagctgtgt ctgcgtctgc tgcg 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
cgcggcactg atccccacag gtgatgggca gaatctgttt acgaaagacg 50

<210> 68
<211> 2555
<212> DNA
<213> Homo Sapien

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ccctctgctg ctgcgcgtgc tctgctact ggccctgggg cctgggggtgc 200
agggctgccc atccggctgc cagtgcagcc agccacagac agtcttctgc 250
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ttgccggcct gccgggcctg cagctcctgg acctgtcaca gaaccagatc 400

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 catgttttgc ttttttaaaa tatatatata tttataagag atcctttccc 2450
 atttattctg ggaagatgtt tttcaaactc agagacaagg actttggttt 2500
 ttgtaagaca aacgatgata tgaaggcctt ttgtaagaaa aaataaaaaa 2550
 aaaaa 2555

<210> 69
 <211> 598
 <212> PRT
 <213> Homo Sapien

<400> 69
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 20 25 30
 Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr
 35 40 45
 Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe
 50 55 60
 Glu Asn Gly Ile Thr Met Leu Asp Ala Ser Ser Phe Ala Gly Leu
 65 70 75
 Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser
 80 85 90
 Leu Arg Leu Pro Arg Leu Leu Leu Leu Asp Leu Ser His Asn Ser
 95 100 105
 Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala Asn Val Glu

110	115	120
Ala Leu Arg Leu	Ala Gly Leu Gly Leu Gln Gln Leu Asp Glu Gly	
125	130	135
Leu Phe Ser Arg	Leu Arg Asn Leu His Asp Leu Asp Val Ser Asp	
140	145	150
Asn Gln Leu Glu	Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly	
155	160	165
Leu Thr Arg Leu	Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu	
170	175	180
Arg Pro Glu Asp	Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp	
185	190	195
Val Ser Asn Leu	Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly	
200	205	210
Leu Phe Pro Arg	Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe	
215	220	225
Asn Cys Val Cys	Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu	
230	235	240
Ser His Val Thr	Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe	
245	250	255
Pro Pro Lys Asn	Ala Gly Arg Leu Leu Leu Glu Leu Asp Tyr Ala	
260	265	270
Asp Phe Gly Cys	Pro Ala Thr Thr Thr Thr Ala Thr Val Pro Thr	
275	280	285
Thr Arg Pro Val	Val Arg Glu Pro Thr Ala Leu Ser Ser Ser Leu	
290	295	300
Ala Pro Thr Trp	Leu Ser Pro Thr Ala Pro Ala Thr Glu Ala Pro	
305	310	315
Ser Pro Pro Ser	Thr Ala Pro Pro Thr Val Gly Pro Val Pro Gln	
320	325	330
Pro Gln Asp Cys	Pro Pro Ser Thr Cys Leu Asn Gly Gly Thr Cys	
335	340	345
His Leu Gly Thr	Arg His His Leu Ala Cys Leu Cys Pro Glu Gly	
350	355	360
Phe Thr Gly Leu	Tyr Cys Glu Ser Gln Met Gly Gln Gly Thr Arg	
365	370	375
Pro Ser Pro Thr	Pro Val Thr Pro Arg Pro Pro Arg Ser Leu Thr	
380	385	390
Leu Gly Ile Glu	Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu	
395	400	405

Gln Arg Tyr Leu	Gln Gly Ser Ser Val	Gln Leu Arg Ser Leu Arg
410	415	420
Leu Thr Tyr Arg	Asn Leu Ser Gly Pro	Asp Lys Arg Leu Val Thr
425	430	435
Leu Arg Leu Pro	Ala Ser Leu Ala Glu	Tyr Thr Val Thr Gln Leu
440	445	450
Arg Pro Asn Ala	Thr Tyr Ser Val Cys	Val Met Pro Leu Gly Pro
455	460	465
Gly Arg Val Pro	Glu Gly Glu Glu Ala	Cys Gly Glu Ala His Thr
470	475	480
Pro Pro Ala Val	His Ser Asn His Ala	Pro Val Thr Gln Ala Arg
485	490	495
Glu Gly Asn Leu	Pro Leu Leu Ile Ala	Pro Ala Leu Ala Ala Val
500	505	510
Leu Leu Ala Ala	Leu Ala Ala Val Gly	Ala Ala Tyr Cys Val Arg
515	520	525
Arg Gly Arg Ala	Met Ala Ala Ala Ala	Gln Asp Lys Gly Gln Val
530	535	540
Gly Pro Gly Ala	Gly Pro Leu Glu Leu	Glu Gly Val Lys Val Pro
545	550	555
Leu Glu Pro Gly	Pro Lys Ala Thr Glu	Gly Gly Gly Glu Ala Leu
560	565	570
Pro Ser Gly Ser	Glu Cys Glu Val Pro	Leu Met Gly Phe Pro Gly
575	580	585
Pro Gly Leu Gln	Ser Pro Leu His Ala	Lys Pro Tyr Ile
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<210> 70

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

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<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<400> 71
cggttctggg gacgttaggg ctcg 24

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 72
ctgcccacgg tccacctgcc tcaat 25

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 73
aggactgccc accgtccacc tgcctcaatg ggggcacatg ccacc 45

<210> 74
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 74
acgcaaagcc ctacatctaa gccagagaga gacagggcag ctggg 45

<210> 75
<211> 1077
<212> DNA
<213> Homo Sapien

<400> 75
ggcactagga caaccttctt cctttctgca ccaactgcccg tacccttacc 50
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 cttgcttctg ttccccatgg agctccg 1077

<210> 76
 <211> 250
 <212> PRT
 <213> Homo Sapien

<400> 76
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 Leu Trp Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala
 35 40 45
 Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg
 50 55 60
 Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly
 65 70 75
 Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala
 80 85 90
 Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala
 95 100 105
 Val Leu Thr Gln Lys Gln Lys Lys Gln His Ser Val Leu His Leu
 110 115 120

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<210> 78

<211> 281

<212> PRT

<213> Homo Sapien

<400> 78

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				20					25				30	
Gln	Gly	Glu	Gln	Gln	Glu	Trp	Glu	Gly	Thr	Glu	Glu	Leu	Pro	Ser
				35					40				45	
Pro	Pro	Asp	His	Ala	Glu	Arg	Ala	Glu	Glu	Gln	His	Glu	Lys	Tyr
				50					55				60	
Arg	Pro	Ser	Gln	Asp	Gln	Gly	Leu	Pro	Ala	Ser	Arg	Cys	Leu	Arg
				65					70				75	
Cys	Cys	Asp	Pro	Gly	Thr	Ser	Met	Tyr	Pro	Ala	Thr	Ala	Val	Pro
				80					85				90	
Gln	Ile	Asn	Ile	Thr	Ile	Leu	Lys	Gly	Glu	Lys	Gly	Asp	Arg	Gly
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Asp	Arg	Gly	Leu	Gln	Gly	Lys	Tyr	Gly	Lys	Thr	Gly	Ser	Ala	Gly

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125	130	135
Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val		
140	145	150
Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val		
155	160	165
Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met		
170	175	180
Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe		
185	190	195
Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His		
200	205	210
Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val		
215	220	225
Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu		
230	235	240
Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg		
245	250	255
Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe		
260	265	270
Ser Gly Tyr Leu Val Lys His Ala Thr Glu Pro		
275	280	

<210> 79
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 79
 tacaggccca gtcaggacca gggg 24

<210> 80
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 80
 ctgaagaagt agaggccggg cacg 24

<210> 81

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
cccgggtgctt gcgctgctgt gaccccggtg cctccatgta cccgg 45

<210> 82
<211> 2284
<212> DNA
<213> Homo Sapien

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ggcgccgggg tctctcgac gccagagaga aatctcatca tctgtgcagc 150
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cttcccagcc acagctggcc accacagctc cacctgtaac cactgtcact 1050

Ile	Cys	Phe	Leu	Thr	Leu	Arg	Leu	Ser	Ala	Ser	Gln	Asn	Cys	Leu	20	25	30
Lys	Lys	Ser	Leu	Glu	Asp	Val	Val	Ile	Asp	Ile	Gln	Ser	Ser	Leu	35	40	45
Ser	Lys	Gly	Ile	Arg	Gly	Asn	Glu	Pro	Val	Tyr	Thr	Ser	Thr	Gln	50	55	60
Glu	Asp	Cys	Ile	Asn	Ser	Cys	Cys	Ser	Thr	Lys	Asn	Ile	Ser	Gly	65	70	75
Asp	Lys	Ala	Cys	Asn	Leu	Met	Ile	Phe	Asp	Thr	Arg	Lys	Thr	Ala	80	85	90
Arg	Gln	Pro	Asn	Cys	Tyr	Leu	Phe	Phe	Cys	Pro	Asn	Glu	Glu	Ala	95	100	105
Cys	Pro	Leu	Lys	Pro	Ala	Lys	Gly	Leu	Met	Ser	Tyr	Arg	Ile	Ile	110	115	120
Thr	Asp	Phe	Pro	Ser	Leu	Thr	Arg	Asn	Leu	Pro	Ser	Gln	Glu	Leu	125	130	135
Pro	Gln	Glu	Asp	Ser	Leu	Leu	His	Gly	Gln	Phe	Ser	Gln	Ala	Val	140	145	150
Thr	Pro	Leu	Ala	His	His	His	Thr	Asp	Tyr	Ser	Lys	Pro	Thr	Asp	155	160	165
Ile	Ser	Trp	Arg	Asp	Thr	Leu	Ser	Gln	Lys	Phe	Gly	Ser	Ser	Asp	170	175	180
His	Leu	Glu	Lys	Leu	Phe	Lys	Met	Asp	Glu	Ala	Ser	Ala	Gln	Leu	185	190	195
Leu	Ala	Tyr	Lys	Glu	Lys	Gly	His	Ser	Gln	Ser	Ser	Gln	Phe	Ser	200	205	210
Ser	Asp	Gln	Glu	Ile	Ala	His	Leu	Leu	Pro	Glu	Asn	Val	Ser	Ala	215	220	225
Leu	Pro	Ala	Thr	Val	Ala	Val	Ala	Ser	Pro	His	Thr	Thr	Ser	Ala	230	235	240
Thr	Pro	Lys	Pro	Ala	Thr	Leu	Leu	Pro	Thr	Asn	Ala	Ser	Val	Thr	245	250	255
Pro	Ser	Gly	Thr	Ser	Gln	Pro	Gln	Leu	Ala	Thr	Thr	Ala	Pro	Pro	260	265	270
Val	Thr	Thr	Val	Thr	Ser	Gln	Pro	Pro	Thr	Thr	Leu	Ile	Ser	Thr	275	280	285
Val	Phe	Thr	Arg	Ala	Ala	Ala	Thr	Leu	Gln	Ala	Met	Ala	Thr	Thr	290	295	300
Ala	Val	Leu	Thr	Thr	Thr	Phe	Gln	Ala	Pro	Thr	Asp	Ser	Lys	Gly			

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<220>
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<220>
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<210> 89
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<210> 90
 <211> 957
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 gtcttcgcct ccttggtgtg ctggtattcg gggtagctgc tcgagagct 100
 cattccagat gcaccctgt ccagtgtgc ctatagcatc cgcagcatcg 150
 gggagaggcc tgtcctcaaa gctccagtcc caaaaggca aaaatgtgac 200
 cactggactc cctgcccata tgacacctat gctacaggt tactcagcgg 250
 aggtggcaga agcaagtacg ccaaaatctg ctttgaggat aacactactta 300
 tgggagaaca gctgggaaat gttgccagag gaataaacat tgccattgtc 350
 aactatgtaa ctgggaatgt gacagcaaca cgatgttttg atatgtatga 400
 aggcgataac tctggaccga tgacaaagtt tattcagagt gctgctccaa 450
 aatccctgct cttcatggtg acctatgacg acggaagcac aagactgaat 500

Variable	Mean	SD	Min	Max
Age	34.5	10.2	22	55
Gender	Male	Female		
Marital status	Married	Single		
Education	High school	College		
Occupation	Manager	Worker		
Income	Low	High		
Health status	Good	Poor		
Smoking status	Smoker	Non-smoker		
Alcohol consumption	Regular	Occasional		
Exercise frequency	High	Low		
Stress level	High	Low		
Sleep quality	Good	Poor		
Dietary habits	Healthy	Unhealthy		
Family size	Small	Large		
Work-life balance	Good	Poor		
Life satisfaction	High	Low		
Overall well-being	Good	Poor		

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Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val
  1          5          10          15

Phe Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu
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Leu Ile Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg
          35          40          45

Ser Ile Gly Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg
          50          55          60

Gln Lys Cys Asp His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala
          65          70          75

Tyr Arg Leu Leu Ser Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile
          80          85          90

Cys Phe Glu Asp Asn Leu Leu Met Gly Glu Gln Leu Gly Asn Val
          95          100          105

Ala Arg Gly Ile Asn Ile Ala Ile Val Asn Tyr Val Thr Gly Asn
          110          115          120

Val Thr Ala Thr Arg Cys Phe Asp Met Tyr Glu Gly Asp Asn Ser
          125          130          135

Gly Pro Met Thr Lys Phe Ile Gln Ser Ala Ala Pro Lys Ser Leu
          140          145          150

Leu Phe Met Val Thr Tyr Asp Asp Gly Ser Thr Arg Leu Asn Asn
          155          160          165

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Asp	Ala	Lys	Asn	Ala	Ile	Glu	Ala	Leu	Gly	Ser	Lys	Glu	Ile	Arg
									170					180
Asn	Met	Lys	Phe	Arg	Ser	Ser	Trp	Val	Phe	Ile	Ala	Ala	Lys	Gly
									185					195
Leu	Glu	Leu	Pro	Ser	Glu	Ile	Gln	Arg	Glu	Lys	Ile	Asn	His	Ser
									200					210
Asp	Ala	Lys	Asn	Asn	Arg	Tyr	Ser	Gly	Trp	Pro	Ala	Glu	Ile	Gln
									215					225
Ile	Glu	Gly	Cys	Ile	Pro	Lys	Glu	Arg	Ser					
									230					235

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<400> 93

aggcttgga ctccttc 18

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aagattcttg agcgattcca gctg 24

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<212> DNA

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cctcgggtctc ctcattctgtg a 21

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tggcccagct gacgagccct 20

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<211> 21

<212> DNA

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<211> 30

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<400> 109

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<210> 110

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<220>

<223> Synthetic oligonucleotide probe

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<210> 111

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

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<400> 111

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<220>

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<210> 114

<211> 48

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<213> Artificial Sequence

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